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## SEQUENCE LISTING

<110> Bogosian, Gregg  
O'Neill, Julia P.  
Smith, Hong Q.

<120> Prevention of Incorporation of Non-Standard Amino Acids into  
Protein

<130> 11916.0059.00PC00

<150> US 60/505,807

<151> 2003-09-25

<160> 16

<170> PatentIn version 3.3

<210> 1

<211> 1344

<212> DNA

<213> Escherichia coli

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atccagtttc gcgtggtatg ggttgatgat cgcaaccaga tacagggtcaa ccgtgcatgg 240  
cgtgtgcagt tcagctctgc catcgcccg tacaaggcg gtatgcgctt ccatccgtca 300  
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cgtcttatcg aaatcaaagc cagccgcgat ggtcagatgg cagattacgc caaagaattt 900  
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- 2 -

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&lt;210&gt; 2

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 2

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 Thr Thr Leu Trp Pro Phe Leu Glu Gln Asn Pro Lys Tyr Arg Gln Met  
 35 40 45  
 Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg  
 50 55 60  
 Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp  
 65 70 75 80  
 Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Met Arg  
 85 90 95  
 Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu  
 100 105 110  
 Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys  
 115 120 125  
 Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met  
 130 135 140  
 Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala  
 145 150 155 160  
 Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val  
 165 170 175

- 3 -

Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys  
 180 185 190  
 Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro  
 195 200 205  
 Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys  
 210 215 220  
 Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser  
 225 230 235 240  
 Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala  
 245 250 255  
 Arg Val Ile Thr Ala Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ser  
 260 265 270  
 Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser  
 275 280 285  
 Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr  
 290 295 300  
 Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro  
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 Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile  
 325 330 335  
 Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr  
 340 345 350  
 Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro  
 355 360 365  
 Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met  
 370 375 380  
 Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala  
 385 390 395 400  
 Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His  
 405 410 415  
 Gly Gly Glu Gly Glu Gln Thr Asn Tyr Val Gln Gly Ala Asn Ile Ala  
 420 425 430  
 Gly Phe Val Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile  
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&lt;210&gt; 3

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

- 4 -

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atccagtttc gcgtgggatg ggttgatgat cgcaaccaga tacaggtcaa ccgtgcatgg      240
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gttaaccttt ccattctcaa attcctcggc tttgaacaaa ctttcaaaaa tgccctgact      360
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ggtgaagtga tgcgtttttg ccaggcgctg atgactgaac tgtatcgcca cctgggcgcg      480
gataccgacg ttccggcagg tgatatcggg gttggtggtc gtgaagtcgg ctttatggcg      540
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tttggcggca gtcttattcg cccggaagct accggctacg gtctggttta tttcacagaa      660
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caggcaggcg tactatttgc accgggtaaa gcggctaata ctggtggcgt cgctacatcg      1140
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cgtttgcatc acatcatgct ggatatccac catgcctgtg ttgagcatgg tggatgaagg      1260
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&lt;210&gt; 4

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 4

- 5 -

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 Thr Thr Leu Trp Pro Phe Leu Glu Gln Asn Pro Lys Tyr Arg Gln Met  
 35 40 45  
 Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg  
 50 55 60  
 Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp  
 65 70 75 80  
 Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Leu Gly Gly Met Arg  
 85 90 95  
 Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu  
 100 105 110  
 Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys  
 115 120 125  
 Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met  
 130 135 140  
 Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala  
 145 150 155 160  
 Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val  
 165 170 175  
 Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys  
 180 185 190  
 Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro  
 195 200 205  
 Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys  
 210 215 220  
 Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser  
 225 230 235 240  
 Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala  
 245 250 255  
 Arg Val Ile Thr Ala Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ser  
 260 265 270  
 Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser  
 275 280 285  
 Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr

- 6 -

290	295	300
Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro		
305	310	315 320
Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile		
	325	330 335
Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr		
	340	345 350
Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro		
	355	360 365
Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met		
	370	375 380
Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala		
385	390	395 400
Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His		
	405	410 415
Gly Gly Glu Gly Glu Gln Thr Asn Tyr Val Gln Gly Ala Asn Ile Ala		
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 <213> Bacillus cereus

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 ttgcgtcttg caaaagggat gacatacaaa aacgcagcag ctggttttaa cttaggtggt 240  
 gcgaaaacag taattatcgg tgatcctcgt aaagataaga gcgaagcaat gttccgtgca 300  
 ctaggacgtt atatccaagg actaaacgga cgttacatta cagctgaaga tggttggtaca 360  
 acagtagatg atatggatat tatccatgaa gaaactgact ttgtaacagg tatctcacca 420  
 tcattcgggtt cttctggtaa cccatctccg gtaactgcat acggtgttta ccgtgggtatg 480  
 aaagcagctg caaaagaagc ttctgggtact gacaatttag aaggaaaagt aattgctggt 540  
 caaggcggtg gtaacgtagc atatcaccta tgcaaacatt tacacgctga aggagcaaaa 600

- 7 -

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tcagcagttg aaccaaataa aattttacggg gttgaatgcg atattttacgc accatgtgca    720
ctaggcgcaa cagttaatga tgaaactatt ccacaactta aagcaaaaagt aatcgcaggt    780
tctgcaaata accaattaaa agaagatcgt catgggtgaca tcattcatga aatgggtatt    840
gtatacgcac cagattatgt aattaatgca ggtggcgtaa ttaacgtagc agacgaatta    900
tatggataca atagagaacg tgcactaaaa cgtgttgagt ctatttatga cagcattgca    960
aaagtaatcg aaatttcaaa acgcgatggc atagcaactt atgtagcggc agatcgtcta   1020
gctgaagagc gcattgcaag cttgaagaat tctcgtagca cttacttacg caacgggtcac   1080
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&lt;210&gt; 6

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Bacillus cereus

&lt;400&gt; 6

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Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1           5           10           15

```

```

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
          20           25           30

```

```

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
          35           40           45

```

```

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
          50           55           60

```

```

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65           70           75           80

```

```

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
          85           90           95

```

```

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
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```

```

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
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```

```

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
          130          135          140

```

```

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145          150          155          160

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- 8 -

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys  
 165 170 175  
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys  
 180 185 190  
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys  
 195 200 205  
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu  
 210 215 220  
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala  
 225 230 235 240  
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys  
 245 250 255  
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly  
 260 265 270  
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile  
 275 280 285  
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn  
 290 295 300  
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala  
 305 310 315 320  
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala  
 325 330 335  
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg  
 340 345 350  
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg  
 355 360 365

&lt;210&gt; 7

&lt;211&gt; 1098

&lt;212&gt; DNA

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 7

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 ggcggaacga gaatgtggac atatgaaaat gaagaagcgg caattgaaga cgcgctcaga 180  
 ctggcaagag gcatgacctt taaagacgcg gctgcaggcc taaaccttgg cggcggaataa 240  
 acagtaataa tcggcgatcc acgcaaagac aaaaatgaag aaatgttccg cgcgtttggc 300



- 9 -

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 gaggatatgg acattattca tgatgaaaca gactatgtca cagggatttc tcctgctttc 420  
 ggctcttctg gaaatccatc tccagttaca gcgtacgggg tgtacagagg aatgaaagca 480  
 gccgctaaag ctgctttcgg aaccgactct cttgaaggga aaaccatcgc tgtacagggt 540  
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 cttgagattt ctcagcgtga cggcattcca acatatttag cagctgaccg cttggcagag 1020  
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&lt;210&gt; 8

&lt;211&gt; 364

&lt;212&gt; PRT

<213> *Bacillus subtilis*

&lt;400&gt; 8

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 20 25 30  
 Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr  
 35 40 45  
 Glu Asn Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly  
 50 55 60  
 Met Thr Tyr Lys Asp Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys  
 65 70 75 80  
 Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe  
 85 90 95  
 Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr  
 100 105 110

- 10 -

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His Asp  
 115 120 125  
 Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly  
 130 135 140  
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala  
 145 150 155 160  
 Ala Ala Lys Ala Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Ile  
 165 170 175  
 Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu  
 180 185 190  
 His Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Lys Gln Ser  
 195 200 205  
 Val Gln Arg Ala Val Glu Asp Phe Gly Ala Arg Ala Val Asp Pro Glu  
 210 215 220  
 Glu Ile Tyr Ser Gln Glu Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly  
 225 230 235 240  
 Ala Thr Ile Asn Asp Asp Thr Ile Lys Gln Leu Lys Ala Lys Val Ile  
 245 250 255  
 Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Gln  
 260 265 270  
 Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala  
 275 280 285  
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Ala Glu  
 290 295 300  
 Arg Ala Leu Lys Lys Val Glu Gly Ile Tyr Gly Asn Ile Glu Arg Val  
 305 310 315 320  
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 <211> 1062  
 <212> DNA  
 <213> Nostoc sp.

<400> 9

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ttgagtcggg ggatgactta taaagcagct tgcgctaaca ttcccgcagg cggaggcaaa      240
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tttgtggaaa gtctcaaagg tagatttatt accgggcaag atgtgaatat cactccacaa      360
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agttctgaaa aaacagcaga aataaaacac ctttttggtg ctacagtagt agagccagat      660
gaaatttact cacaaaatgt agacatat ttccctgtg ctatgggagg aattattaac      720
agtcaaacia ttcccact acaagccaaa attattgctg gtgctgccaa taaccagtta      780
gataatgagc gtctgcatgg tcaaagatta gtagaaaaag atatcctcta ctgtcctgat      840
tatgtaatca atgctgggtg tatcatcaac gtttataacg aaatgattgg ctatgaagaa      900
gataaggcct tcaagcaagt taataatatt tacgacacat tattagcaat tttcaatatt      960
gctcaacaac aaagcattac tactaatgat gcttcaaac ggcttgacaga tgaaaggatt     1020
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<210> 10  
 <211> 353  
 <212> PRT  
 <213> Nostoc sp.

<400> 10

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Met Gln Leu Phe Glu Thr Val Arg Glu Met Gly His Glu Gln Val Leu
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Tyr Cys His Gly Lys Asn Pro Asp Ile Arg Ala Ile Ile Ala Ile His
          20           25           30

```

```

Asp Thr Thr Leu Gly Pro Ala Met Gly Ala Thr Arg Leu Tyr Pro Tyr
          35           40           45

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```

Ile Asn Glu Glu Ala Ala Leu Arg Asp Ala Leu Arg Leu Ser Arg Gly
50           55           60

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- 12 -

Met	Thr	Tyr	Lys	Ala	Ala	Cys	Ala	Asn	Ile	Pro	Ala	Gly	Gly	Gly	Lys	65	70	75	80
Ala	Val	Ile	Ile	Ala	Asn	Pro	Glu	Asp	Lys	Thr	Asp	Glu	Met	Leu	Arg		85	90	95
Ala	Tyr	Gly	Arg	Phe	Val	Glu	Ser	Leu	Lys	Gly	Arg	Phe	Ile	Thr	Gly		100	105	110
Gln	Asp	Val	Asn	Ile	Thr	Pro	Gln	Asp	Val	Arg	Thr	Ile	Lys	Gln	Glu		115	120	125
Thr	Asn	Tyr	Val	Val	Gly	Val	Glu	Glu	Lys	Ser	Gly	Gly	Pro	Ala	Pro		130	135	140
Ile	Thr	Ala	Leu	Gly	Val	Phe	Leu	Gly	Ile	Lys	Ala	Ala	Val	Glu	Phe	145	150	155	160
Arg	Trp	Gln	Thr	Lys	Asn	Ile	Glu	Gly	Met	Thr	Val	Ala	Val	Gln	Gly		165	170	175
Leu	Gly	Asn	Val	Gly	Gln	Asn	Leu	Cys	Arg	His	Leu	His	Glu	Asn	Gly		180	185	190
Ile	Lys	Leu	Ile	Val	Ala	Asp	Phe	Ser	Ser	Glu	Lys	Thr	Ala	Glu	Ile		195	200	205
Lys	His	Leu	Phe	Gly	Ala	Thr	Val	Val	Glu	Pro	Asp	Glu	Ile	Tyr	Ser	210	215	220	
Gln	Asn	Val	Asp	Ile	Phe	Ser	Pro	Cys	Ala	Met	Gly	Gly	Ile	Ile	Asn	225	230	235	240
Ser	Gln	Thr	Ile	Pro	Gln	Leu	Gln	Ala	Lys	Ile	Ile	Ala	Gly	Ala	Ala		245	250	255
Asn	Asn	Gln	Leu	Asp	Asn	Glu	Arg	Leu	His	Gly	Gln	Arg	Leu	Val	Glu		260	265	270
Lys	Asp	Ile	Leu	Tyr	Cys	Pro	Asp	Tyr	Val	Ile	Asn	Ala	Gly	Gly	Ile		275	280	285
Ile	Asn	Val	Tyr	Asn	Glu	Met	Ile	Gly	Tyr	Glu	Glu	Asp	Lys	Ala	Phe	290	295	300	
Lys	Gln	Val	Asn	Asn	Ile	Tyr	Asp	Thr	Leu	Leu	Ala	Ile	Phe	Asn	Ile	305	310	315	320
Ala	Gln	Gln	Gln	Ser	Ile	Thr	Thr	Asn	Asp	Ala	Ser	Lys	Arg	Leu	Ala		325	330	335
Asp	Glu	Arg	Ile	Met	Lys	Ala	Arg	Ile	Asn	Lys	Asn	Gln	Leu	Ile	Ala		340	345	350
Ala																			

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<210> 11  
 <211> 1044  
 <212> DNA  
 <213> *Shewanella oneidensis*

<400> 11  
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 aaagaaagtg gcttaaaagc cattattgcc atccataata ccaatttagg ccctgctgtg 120  
 ggtggatgcc ggatgtggaa ctaccaatcc gatgacgaag ccctgacaga cgtattacgc 180  
 ctctcccgtg gtatgactta caaaaacgcg ctcgctgggt taaccatggg cgggtggtaaa 240  
 tcagtgatta ttgccgatcc taagcgccct gaccgcgaag ccctcttccg tgcttttggc 300  
 cgttttatca atagtctcgg tggacgttac tattccgcag aagacgttgg caccacgaca 360  
 gctgatatta tgatcgccca tcaagaaacg ccctatatgg cggggcctga aggcaagagt 420  
 ggcgatcctt ctccgtttac ggcactaggt acttatttag gtatcaaggc cgcggttaaa 480  
 cataagctcg atttagacag cttaaagggc cttaagatcg ccgttcaagg tgttggccat 540  
 gtgggttatt atctgtgtaa acatctacat gaagaagggt cacagctaatt tgttaccgat 600  
 attcatcagg cgtcacttga taaagtgggt accgactttg gtgctaccgt tgttgcacca 660  
 caggatatct acgccaaga cgtcgatgtg tacgccccat gcgcactagg tgcgacctta 720  
 aacgatgtta ccctgccact actcaaagct aagattgttg caggttgtgc caacaaccaa 780  
 ttagccgaag tacgccatgg cgagcagtta aaagaaatgg gcattcttta tgcgccagat 840  
 tatgtgatta acgcgggcgg cattattaac gtatcattcg aaaaagacta tgatgcggcg 900  
 aaatcagaag ctaaggtcag agaaatctac aacacgctgc tgaagatttt tgctaaagcc 960  
 gatgctgaga accgcacgac aggtgcagta gctgacgaaa tggcccgtgc aatttaccaa 1020  
 gcgccaaagc ctaatagggc ttag 1044

<210> 12  
 <211> 347  
 <212> PRT  
 <213> *Shewanella oneidensis*

<400> 12

Met Ala Val Phe Asn His Val Ser Phe Asp Glu His Glu Gln Val Val  
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Phe Cys His Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His

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Asn	Thr	Asn	Leu	Gly	Pro	Ala	Val	Gly	Gly	Cys	Arg	Met	Trp	Asn	Tyr
		35					40					45			
Gln	Ser	Asp	Asp	Glu	Ala	Leu	Thr	Asp	Val	Leu	Arg	Leu	Ser	Arg	Gly
	50					55					60				
Met	Thr	Tyr	Lys	Asn	Ala	Leu	Ala	Gly	Leu	Thr	Met	Gly	Gly	Gly	Lys
65						70					75				80
Ser	Val	Ile	Ile	Ala	Asp	Pro	Lys	Arg	Pro	Asp	Arg	Glu	Ala	Leu	Phe
				85					90					95	
Arg	Ala	Phe	Gly	Arg	Phe	Ile	Asn	Ser	Leu	Gly	Gly	Arg	Tyr	Tyr	Ser
			100					105					110		
Ala	Glu	Asp	Val	Gly	Thr	Thr	Thr	Ala	Asp	Ile	Met	Ile	Ala	His	Gln
		115					120					125			
Glu	Thr	Pro	Tyr	Met	Ala	Gly	Leu	Glu	Gly	Lys	Ser	Gly	Asp	Pro	Ser
	130					135					140				
Pro	Phe	Thr	Ala	Leu	Gly	Thr	Tyr	Leu	Gly	Ile	Lys	Ala	Ala	Val	Lys
145						150					155				160
His	Lys	Leu	Asp	Leu	Asp	Ser	Leu	Lys	Gly	Leu	Lys	Ile	Ala	Val	Gln
			165						170					175	
Gly	Val	Gly	His	Val	Gly	Tyr	Tyr	Leu	Cys	Lys	His	Leu	His	Glu	Glu
			180					185					190		
Gly	Ala	Gln	Leu	Ile	Val	Thr	Asp	Ile	His	Gln	Ala	Ser	Leu	Asp	Lys
		195					200					205			
Val	Ala	Thr	Asp	Phe	Gly	Ala	Thr	Val	Val	Ala	Pro	Gln	Asp	Ile	Tyr
	210					215					220				
Ala	Gln	Asp	Val	Asp	Val	Tyr	Ala	Pro	Cys	Ala	Leu	Gly	Ala	Thr	Leu
225						230					235				240
Asn	Asp	Val	Thr	Leu	Pro	Leu	Leu	Lys	Ala	Lys	Ile	Val	Ala	Gly	Cys
				245					250					255	
Ala	Asn	Asn	Gln	Leu	Ala	Glu	Val	Arg	His	Gly	Glu	Gln	Leu	Lys	Glu
			260					265					270		
Met	Gly	Ile	Leu	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ala	Gly	Gly	Ile
		275					280					285			
Ile	Asn	Val	Ser	Phe	Glu	Lys	Asp	Tyr	Asp	Ala	Ala	Lys	Ser	Glu	Ala
	290						295				300				
Lys	Val	Arg	Glu	Ile	Tyr	Asn	Thr	Leu	Leu	Lys	Ile	Phe	Ala	Lys	Ala
305						310					315				320

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Asp Ala Glu Asn Arg Thr Thr Gly Ala Val Ala Asp Glu Met Ala Arg  
325 330 335

Ala Ile Tyr Gln Ala Pro Lys Pro Asn Arg Ala  
340 345

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<210> 13
<211> 1086
<212> DNA
<213> Streptomyces avermitilis
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gagcaagtgc	tgtcttgcca	ggaccggggc	actggtctca	aggccgtcat	cgccatccac		120
tccaccgccc	tgggccccgc	cctcggcggg	acgcgcttct	acccgtacgc	gagcgaggag		180
gaggccgtcg	ccgacgcgct	gaacctcgcg	cgcgggatgt	cgtacaagaa	cgccatggcc		240
ggcctcgacc	acggcgggcg	caaggccgtc	atcatcggtg	accccgagcg	gatcaagacc		300
gaggagctgc	tgttggccta	cggccgggtt	gtggcctcgc	tcggcggggc	gtacgtcacc		360
gcgtgcgacg	tcggtacgta	cgtcgccgac	atggacgtcg	tggcgcgcga	gtgccgctgg		420
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aaggccgcga	agatcttcga	caccacgctg	gccatattcg	cacgtgcgaa	ggaagacggc		1020
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ggctga							1086

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<210> 14
<211> 361
<212> PRT
<213> Streptomyces avermitilis
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&lt;400&gt; 14

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Gln Gly Gly His Glu Gln Val Val Leu Cys Gln Asp Arg Ala Thr Gly
          20          25          30

Leu Lys Ala Val Ile Ala Ile His Ser Thr Ala Leu Gly Pro Ala Leu
          35          40          45

Gly Gly Thr Arg Phe Tyr Pro Tyr Ala Ser Glu Glu Glu Ala Val Ala
          50          55          60

Asp Ala Leu Asn Leu Ala Arg Gly Met Ser Tyr Lys Asn Ala Met Ala
65          70          75          80

Gly Leu Asp His Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Pro Glu
          85          90          95

Arg Ile Lys Thr Glu Glu Leu Leu Leu Ala Tyr Gly Arg Phe Val Ala
          100          105          110

Ser Leu Gly Gly Arg Tyr Val Thr Ala Cys Asp Val Gly Thr Tyr Val
          115          120          125

Ala Asp Met Asp Val Val Ala Arg Glu Cys Arg Trp Thr Thr Gly Arg
          130          135          140

Ser Pro Glu Asn Gly Gly Ala Gly Asp Ser Ser Val Leu Thr Ala Phe
145          150          155          160

Gly Val Phe Gln Gly Met Arg Ala Ser Ala Gln His Leu Trp Gly Asp
          165          170          175

Pro Thr Leu Arg Gly Arg Lys Val Gly Ile Ala Gly Val Gly Lys Val
          180          185          190

Gly Arg His Leu Val Arg His Leu Leu Asp Asp Gly Ala Glu Val Val
          195          200          205

Ile Thr Asp Val Arg Thr Asp Ser Val Gln Arg Ile Leu Asp Gln His
          210          215          220

Pro Thr Gly Val Thr Ala Val Ala Asp Thr Asp Ala Leu Ile Arg Val
225          230          235          240

Asp Gly Leu Asp Ile Tyr Ala Pro Cys Ala Leu Gly Gly Ala Leu Asn
          245          250          255

Asp Asp Ser Val Thr Val Leu Thr Ala Lys Ile Val Cys Gly Ala Ala
          260          265          270

Asn Asn Gln Leu Ala His Thr Gly Val Glu Lys Asp Leu Ala Asp Arg

```



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275	280	285
Gly Ile Leu Tyr Ala Pro Asp Tyr Val Val Asn Ala Gly Gly Val Ile		
290	295	300
Gln Val Ala Asp Glu Leu His Gly Phe Asp Phe Asp Arg Cys Lys Ala		
305	310	315
Lys Ala Ala Lys Ile Phe Asp Thr Thr Leu Ala Ile Phe Ala Arg Ala		
325	330	335
Lys Glu Asp Gly Ile Pro Pro Ala Ala Ala Asp Arg Ile Ala Glu		
340	345	350
Gln Arg Met Ala Glu Ala Arg Arg Gly		
355	360	

&lt;210&gt; 15

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Nitrosomonas europaea

&lt;400&gt; 15

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cccgaattcc tgcaggccgt ttcagaagtc attgaaagct tgtggccttt tatcgtcgat	120
cattctcggt acgctgagca ggggttgctg gatcggctga tcgagccgga gcgcatgatc	180
atattccggg tggcgtgggt ggatgatcgg ggtgaagtca aggtcaatcg ggggtaccgc	240
attcaatata attcggcgat cggcccatatc aaggggggta cgcgcttcca tccgtcagtc	300
aacctttcca ttctcaaatt ccttgcattt gagcagactt tcaagaatgc actgacaaca	360
ttgccgatgg gaggaggcaa ggggtggatcg gatcttgatc ccaagggtaa aagtcccggg	420
gaaatcatgc gcttctgcca agcgtatgcg gccgaactgt tccggcatgt cgggtgcggat	480
acggatgtac ctgccggaga catcgggtgtg ggcggacggg aagtcgggta catggctggt	540
atgggtcaaga agctgaccaa ccgttcggac tgtgtattta ccggcaaagg attgaccttc	600
gggggatcgc tgctgcccgc ggaagctacc gggtagggtc tgggtctattt tgccgaagag	660
atgctgaatc actccgggtt ttcatgaaa ggcattgcggg tatccgtatc cgggtccggg	720
aacgtggcac agtttgccat tgacaaggcc atgtcgctgg gtgccaaagt agtcacgggt	780
tcagattcga gtggtacggg ggtggatgaa gccggtttta caccagaaaa actggcaatt	840
ctggccgaag tcaagaatcg tctctacggg cgtgtcaatg aatttgctga acgggtggaa	900
gcacagttcc ttccgggtga aaaaccgtgg catgtgccgg tggatgtcgc tttgccctgt	960

- 18 -

gcgacccaga atgaactgaa cgaaaacgac gccgcaatac tgatcaggaa tgggtgcaat 1020  
 tgtgtggccg aggggtgcaa tatgccatgc actgcaggtg ccgtggaacg attccatcat 1080  
 gcgaaagtac tgtttgcacc tggcaaggcg agcaacgcag gcggagtggc tacctcgggt 1140  
 ctggaaatga gccagcaggc catgcgactt tcctggacga gcggagaagt cgatatgcgg 1200  
 ttacaggaaa tcatgcgtgc cattcatcat tcctgcaccg aatacggcaa gaagcctgac 1260  
 ggtacggtca actatgtgga tgggtgccaat gttgccggat ttgtgaaagt ggccgaggca 1320  
 atgctggcgc aaggggtgat ctgataa 1347

&lt;210&gt; 16

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Nitrosomonas europaea

&lt;400&gt; 16

Met Lys Tyr Asn Ser Ile Glu Glu Phe Lys Asn Tyr Val Ser Glu Arg  
 1 5 10 15  
 Asn Pro Gly Gln Pro Glu Phe Leu Gln Ala Val Ser Glu Val Ile Glu  
 20 25 30  
 Ser Leu Trp Pro Phe Ile Val Asp His Ser Arg Tyr Ala Glu Gln Gly  
 35 40 45  
 Leu Leu Asp Arg Leu Ile Glu Pro Glu Arg Met Ile Ile Phe Arg Val  
 50 55 60  
 Ala Trp Val Asp Asp Arg Gly Glu Val Lys Val Asn Arg Gly Tyr Arg  
 65 70 75 80  
 Ile Gln Tyr Asn Ser Ala Ile Gly Pro Tyr Lys Gly Gly Thr Arg Phe  
 85 90 95  
 His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Ala Phe Glu Gln  
 100 105 110  
 Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly  
 115 120 125  
 Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Pro Gly Glu Ile Met Arg  
 130 135 140  
 Phe Cys Gln Ala Tyr Ala Ala Glu Leu Phe Arg His Val Gly Ala Asp  
 145 150 155 160  
 Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val Gly  
 165 170 175  
 Tyr Met Ala Gly Met Val Lys Lys Leu Thr Asn Arg Ser Asp Cys Val

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180						185					190				
Phe	Thr	Gly	Lys	Gly	Leu	Thr	Phe	Gly	Gly	Ser	Leu	Leu	Arg	Pro	Glu
		195					200					205			
Ala	Thr	Gly	Tyr	Gly	Leu	Val	Tyr	Phe	Ala	Glu	Glu	Met	Leu	Asn	His
	210					215					220				
Ser	Gly	Cys	Ser	Leu	Lys	Gly	Met	Arg	Val	Ser	Val	Ser	Gly	Ser	Gly
225					230					235					240
Asn	Val	Ala	Gln	Phe	Ala	Ile	Asp	Lys	Ala	Met	Ser	Leu	Gly	Ala	Lys
				245					250					255	
Val	Val	Thr	Val	Ser	Asp	Ser	Ser	Gly	Thr	Val	Val	Asp	Glu	Ala	Gly
			260					265					270		
Phe	Thr	Pro	Glu	Lys	Leu	Ala	Ile	Leu	Ala	Glu	Val	Lys	Asn	Arg	Leu
		275					280					285			
Tyr	Gly	Arg	Val	Asn	Glu	Phe	Ala	Glu	Arg	Val	Glu	Ala	Gln	Phe	Leu
	290					295					300				
Pro	Gly	Glu	Lys	Pro	Trp	His	Val	Pro	Val	Asp	Val	Ala	Leu	Pro	Cys
305					310					315					320
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Glu	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Arg
				325					330					335	
Asn	Gly	Ala	Asn	Cys	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Cys	Thr	Ala
			340					345					350		
Gly	Ala	Val	Glu	Arg	Phe	His	His	Ala	Lys	Val	Leu	Phe	Ala	Pro	Gly
		355					360					365			
Lys	Ala	Ser	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Gly	Leu	Glu	Met	Ser
	370					375					380				
Gln	Gln	Ala	Met	Arg	Leu	Ser	Trp	Thr	Ser	Gly	Glu	Val	Asp	Met	Arg
385					390					395					400
Leu	Gln	Glu	Ile	Met	Arg	Ala	Ile	His	His	Ser	Cys	Thr	Glu	Tyr	Gly
				405					410					415	
Lys	Lys	Pro	Asp	Gly	Thr	Val	Asn	Tyr	Val	Asp	Gly	Ala	Asn	Val	Ala
			420					425					430		
Gly	Phe	Val	Lys	Val	Ala	Glu	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile	
		435					440					445			